



SEQUENCE LISTING

<110> McKeon, F.
Kayako, K.
Ryeom, S.

<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN,
USES AND REAGENTS RELATED THERETO

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<140> 09/575,580

<141> 2000-05-22

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<170> PatentIn Ver. 2.1

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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
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 Thr Lys Gln Tyr Leu Lys Val Pro Glu Ser Glu Lys Met Phe Leu Ile
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Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val
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His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser
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<213> Mus musculus

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<222> (2410)
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: general
calcineurin antagonist peptide

<220>
<221> SITE
<222> (6)
<223> Xaa=any amino acid residue

<400> 28
Pro Lys Pro Lys Ile Xaa Gln Thr Arg Arg Pro Glu
1 5 10

<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin
antagonist

<400> 29
Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu
1 5 10

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist

<400> 30
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1 5 10

<210> 31
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<212> PRT
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<220>
<223> Description of Artificial Sequence: EGF-derived peptide

<400> 31
Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
1 5 10

<210> 32
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EGF-derived peptide

<400> 32
Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
1 5 10

<210> 33
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pH-dependent membrane-binding internalizing peptide

<220>
<221> SITE
<222> (1)
<223> Xaa=preferably a unique residue, such as Cys or Lys, that facilitates chemical conjugation of the

internalizing peptide to a targeting protein conjugate

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<220>
<221> SITE
<222> (2)..(3)
<223> Xaa=residues selected to modulate the affinity of
      the internalizing peptide for different membranes

<400> 33
Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
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Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
     20          25          30

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide
      substrate

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Gly Asn Ala Ala Ala Ala Arg Arg
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<210> 35
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (4)..(75)

<220>
<223> Description of Artificial Sequence: synthetic
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      Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro
     1           5           10          15

aaa aag aag aag aag gta gct gga ttc
Lys Lys Lys Arg Lys Val Ala Gly Phe
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75

<210> 36
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 36
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 1 5 10 15
 Lys Lys Arg Lys Val Ala Gly Phe
 20

<210> 37
 <211> 225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4) .. (225)

<400> 37
 cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly
 1 5 10 15
 agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96
 Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
 20 25 30
 ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144
 Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr
 35 40 45
 ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln
 50 55 60
 act cat caa gtt tct cta agt aag caa gga ttc 225
 Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe
 65 70

<210> 38
 <211> 74

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: synthetic
 construct

 <400> 38
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 1 5 10 15

 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30

 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
 35 40 45

 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 50 55 60

 His Gln Val Ser Leu Ser Lys Gln Gly Phe
 65 70

<210> 39
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: synthetic
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 <220>
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 <222> (4)...(912)

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 1 5 10 15

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 Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala
 20 25 30

 agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca 144
 Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr
 35 40 45

 cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg 192
 Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser
 50 55 60

 gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg 240
 Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro
 65 70 75

gag gtc ccc cgg acg cgg cgt ccc gtt tcc ggg gcg gtt ttg tcc ggc		288
Glu Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly		
80	85	90
95		
ccg ggg cct gcg cgg gcg cct ccg cca ccc gct ggg tcc gga ggg gcc		336
Pro Gly Pro Ala Arg Ala Pro Pro Pro Ala Gly Ser Gly Gly Ala		
100	105	110
Gly Arg Thr Pro Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val		
115	120	125
gga cgc aca ccc acc acc gcc ccc cgg gcc ccc cga acc cag cgg gtg		384
Gly Arg Thr Pro Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val		
115	120	125
gcg act aag gcc ccc gcg gcc ccg gcg gag acc acc cgc ggc agg		432
Ala Thr Lys Ala Pro Ala Ala Pro Ala Glu Thr Thr Arg Gly Arg		
130	135	140
Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser		
145	150	155
aaa tcg gcc cag cca gaa tcc gcc gca ctc cca gac gcc ccc gcg tcg		480
Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser		
145	150	155
acg gcg cca acc cga tcc aag aca ccc gcg cag ggg ctg gcc aga aag		528
Thr Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys		
160	165	170
175		
ctg cac ttt agc acc gcc ccc cca aac ccc gac gcg cca tgg acc ccc		576
Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro		
180	185	190
cgg gtg gcc ggc ttt aac aag cgc gtc ttc tgc gcc gcg gtc ggg cgc		624
Arg Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg		
195	200	205
ctg gcg gcc atg cat gcc cgg atg gcg gcg gtc cag ctc tgg gac atg		672
Leu Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met		
210	215	220
tcg cgt ccg cgc aca gac gaa gac ctc aac gaa ctc ctt ggc atc acc		720
Ser Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr		
225	230	235
acc atc cgc gtg acg gtc tgc gag ggc aaa aac ctg ctt cag cgc gcc		768
Thr Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala		
240	245	250
255		
aac gag ttg gtg aat cca gac gtg gtg cag gac gtc gac gcg gcc acg		816
Asn Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr		
260	265	270
gcg act cga ggg cgt tct gcg gcg tcg cgc ccc acc gag cga cct cga		864
Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg		
275	280	285
gcc cca gcc cgc tcc gct tct cgc ccc aga cgg ccc gtc gag gaa ttc		912
Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe		
290	295	300

<210> 40
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
construct

<400> 40																
Met	Thr	Ser	Arg	Arg	Ser	Val	Lys	Ser	Gly	Pro	Arg	Glu	Val	Pro	Arg	
1						5				10				15		
Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser																
						20				25				30		
Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg																
						35				40				45		
Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp																
						50				55				60		
Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu																
						65				70				75		80
Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro																
						85				90				95		
Gly Pro Ala Arg Ala Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly																
						100				105				110		
Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val Ala																
						115				120				125		
Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys																
						130				135				140		
Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr																
						145				150				155		160
Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu																
						165				170				175		
His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg																
						180				185				190		
Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu																
						195				200				205		
Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser																
						210				215				220		
Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr																
						225				230				235		240
Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn																
						245				250				255		

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
 260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
 275 280 285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe
 290 295 300

<210> 41
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
 construct

<220>
<221> CDS
<222> (4)..(120)

<400> 41 48
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 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala
 1 5 10 15

tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc 96
 Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg
 20 25 30

ccc aga cgg ccc gtc gag gaa ttc 120
 Pro Arg Arg Pro Val Glu Glu Phe
 35

<210> 42
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
 construct

<400> 42
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
 1 5 10 15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
 20 25 30

Arg Arg Pro Val Glu Glu Phe
 35

<210> 43
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
aggaggtgga tctgc 15

<210> 44
<211> 6
<212> PRT
<213> Mus musculus

<400> 44
Glu Arg Met Arg Arg Pro
1 5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus sequence

<400> 45
Glu Arg Met Pro Pro Arg Arg Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cross-species conserved motif

<220>
<221> MOD_RES
<222> (6)
<223> Variable amino acid

<400> 46
Leu Ile Ser Pro Pro Xaa Ser Pro
1 5

<210> 47
<211> 4

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
      peptide fragment

<220>
<221> MOD_RES
<222> (4)
<223> Any amino acid residue other than Ser or Thr

<400> 47
Arg Arg Pro Xaa
1

<210> 48
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
      peptide fragment

<220>
<221> MOD_RES
<222> (4)
<223> Ala, Gly or Glu

<400> 48
Arg Arg Pro Xaa
1

<210> 49
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
      peptide fragment

<400> 49
Arg Arg Pro Glu
1
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